

FIGURE 1

SEQ ID NO: 1

>STAAU_R009 nucleotide sequence: 1800
TTGCGAATAGATCAATCGATCATTAATGAAATAAAGATAAAAACCGACATTTAGACTTGGTAAGTGAATATGTAAATTAGAAAAAGAG
AGGACGCAATTATATAGGTTTGTCTCTTTTCATGATGAAAGAGACACCTTCATTTACAGTTTCTGAAGATAAACAAATTTGTCAATTGTT
TTGGTTGTAAAAAGGTGGCAATGTTTTCAATTTACTCAAGAAATTAAGACATATCATTTGTTGAAGCGGTTAAAGAAATTAGGTGAT
AGAGTTAATGTTGCTGTAGATATTGAGGCAACACAATCTAACTCAAAATGTTCAAAATGCTGATGATTTACAAATGATTGAAATGCA
TGAGTTAATACAAAGAAATTTTATTATTACGCTTTAACAAAGACAGTCGAAGGCGAACAAGCATTTAAACGTACTTACAAAGAACGTGGTTT
CAGATCGCTTATTAAAGAGCGAGGCATTGGCTTTGCACCCGATAGCTCACATTTTGTGTCATGATTTTCTTCAAAAAAAGGGTTACGAT
ATTGAATTAGCATATGAAGCCGGATTATTATCACGTAAACGAAGAAAATTTTCAGTTATTACGATAGATTTTCGAAATCGTATTATGTTTCC
TTTGAAAAATGCGCAAGGAAGAAATGTTGGATATTTCAGGTCGAACATATACCGGTCAAGAACCAAAATACTTAAATAGTCTGAAACAC
CTATCTTTCAAAAAAGAAAGTTGTTATACAACTTAGATAAAGCGGTAAATCAATTAGAAAAATTAGATGAAATCGTATTACTAGAAAGGT
TTTATGGATGTTATAAAATCTGATACTGCTGGCTTGAAAAACGTTGTTGCAACAATGGGTACACAGTTGTCAAGATGAACATATTACTTT
TATACGAAAGTTAACATCAAAATATAACATTAATGTTTGTGGGATTTTGGCGGTAGTGAAGCAACACTTAAACAGGTCAAAAATTTGT
TACAGCAAGGGCTAAATGTATTTGTTATACAATTTGCCATCAGGCATGGATCCGGATGAATACATTTGTTAAGTATGGCAACGATGCATTT
ACTGCTTTTGTAAAAAATGACAAAAAGTCAATTTGCACATTATAAAGTGAGTATATTAAAGATGAAATTCACACATAATGACCTTTTCATA
TGAACGTTATTTGAAAGAACTAAGTCATGATATTTCGCTTATGAAATCATCGATTTTGCAACAAAAAGGCTTTAAATGATGTTGCACCAT
TTTTCAATGTTAGTCCTGAGCAATTAGCTAACGAAATACAATTCATCAAGCACCCAGCCAATTTATATCCAGAAGATGAGTATGGCGGT
TACATTGAACCTGAGCCAAATTGGTATGGCACAATTTGACAATTTGAGCCGTCAAGAAAAAGCGGAGCGAGCATTTTAAAAACATTTAAT
GAGAGATAAGATACATTTTAAATTTATGAAAGTGTGATAAGGATAACTTCACAAATCAGCATTTTAAATATGTTTCGAAGTCT
TACATGATTTTATGCGGAAAATGATCAATATAATATCAGTGATGCTGTGCAGTATGTTAAATTCAAATGAGTTGAGAGAAAACACTAATT
AGCTTAGAACCAATATAAATTGAATGACGAACCATATGAAAAATGAAATTTGATGATTATGTCAATGTTATTAAATGAAAAAGGACAAGAAAC
AATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTAGAATTACAAAAATACTATTTACAGCAAAATGTTTGCTA
AGAAATAAGAACCGCATGTAG

SEQ ID NO: 2

>STAAU_R009 amino acid sequence : 599
 LRIDQSIINEIKDKTDILDVSEYVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICHCFGCKKGGNVFQFTQEIKDISFVEAVKELGD
 RVNVAVDIEATQSNNSNVQIASDDLQMIEMHELIOEFYYALTKTVEGEQALTYLQERGETDALIKERGIGFAPDSSHCHDFLQKKGYD
 IELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIFQKRKLLYNLDKARKSIRKLDEIVLLEG
 FMDVIKSDTAGLKNVAVATMGTLSDHEITFIRKLTSNITLTFDGFAGSEATLKTGQNLQQLNVFVIQLPSGMDPDEYIGKYGNDAF
 TAFVKNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVSPPEQLANEIQFNQAPANYYPEDEYGG
 YIEPEPIGMAQFDNLSRQEKAEAFILKHLMRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI
 SLEQYNLNDEPYENEIDDYVNVVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAKNKERM

FIGURE 2

SEQ ID NO: 3

>96ORF078 nucleotide sequence
 ATGAATATAATGCAATTCAAAAAGCTTATTGAAATCGATGTATGAAGAGACAAAAGCAAAGC
 GACCCGATTGTAGCAAAATGTATATATCGAGACTGGTTGGCGGTCAATAGATTGTTGGAC
 AATAACGAGTTATCGCCTTTCGATGATTACGACAGAGTTGAAAAGAAAATCATGAATGAA
 ATCAACTGGAAGAAAACACACATTAAAGGAGTGTAA

SEQ ID NO: 4

>96ORF078 amino acid sequence 96_NT|10148-10363|
 MNIMQFKSLLKSMYEETKQSDPIVANVYIETGWAVNRLLDNNELSPFDDYDRVEKKIMNE
 INWKKTHKEC

FIGURE 3

A.

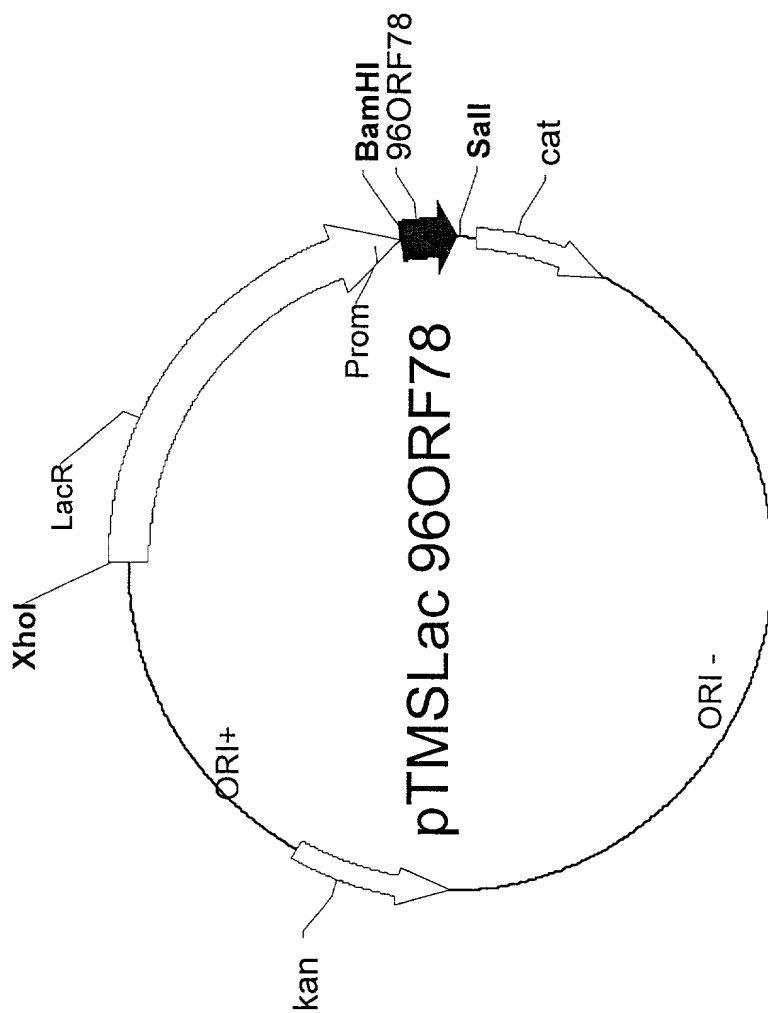


FIGURE 3 B.

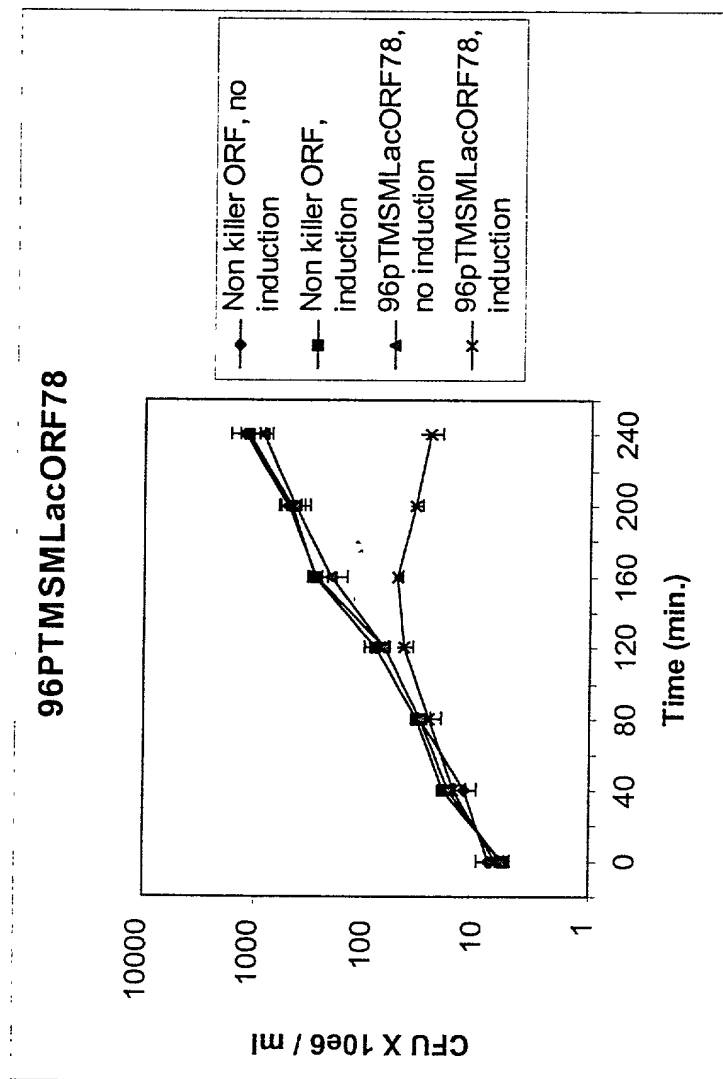
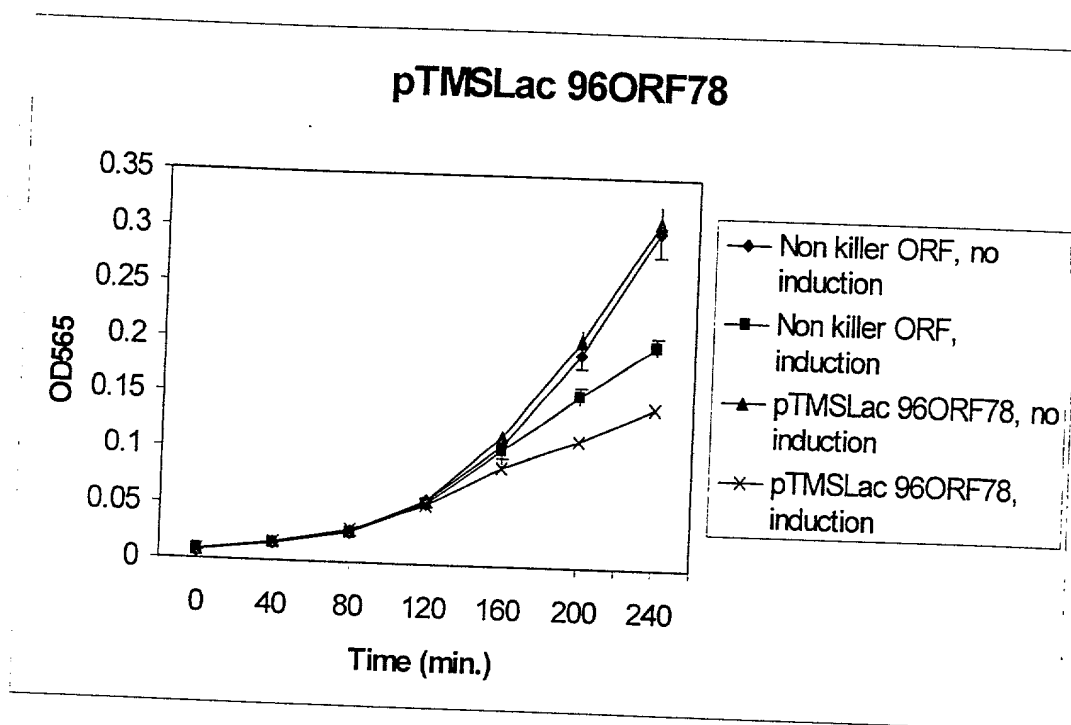


FIGURE 3 C.



D.

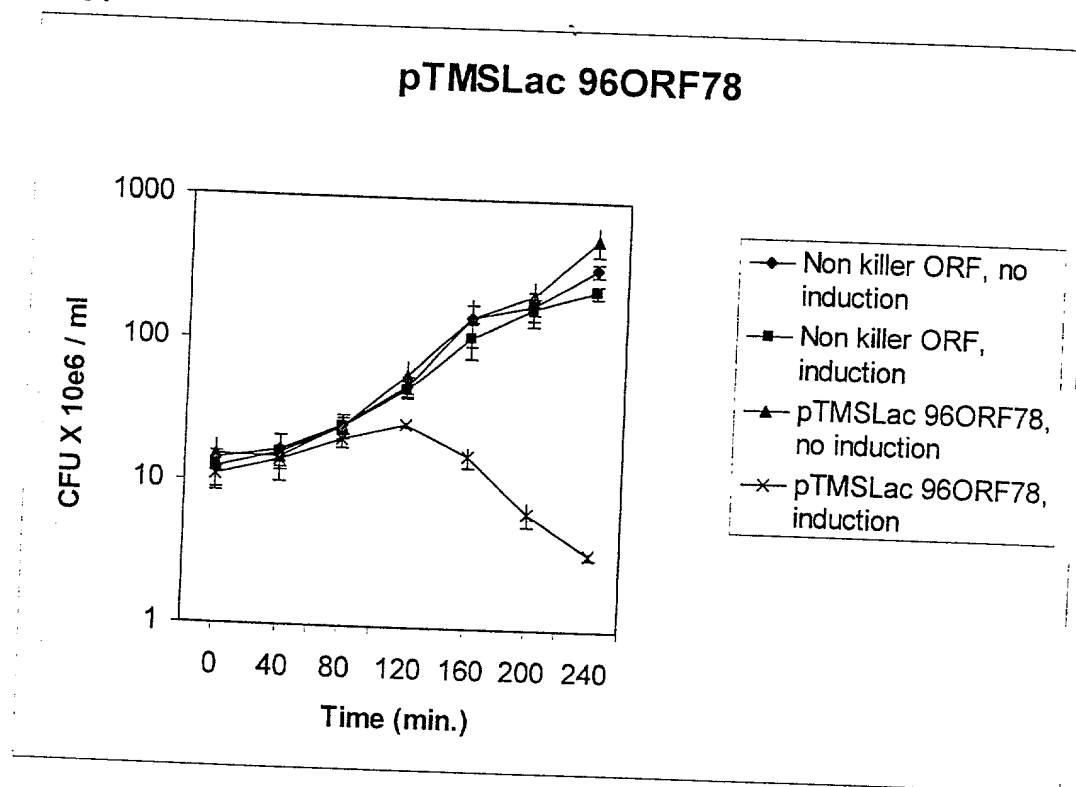


FIGURE 4

A. GST/96ORF78

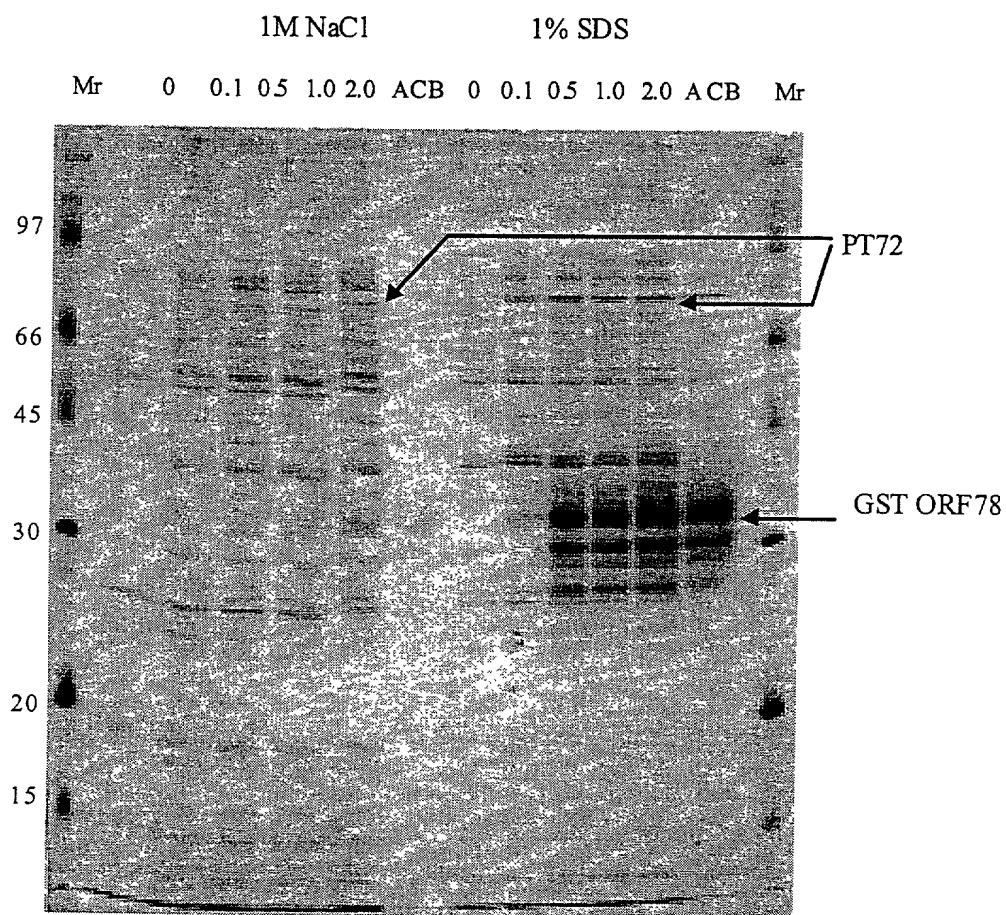


FIGURE 4

B. GST

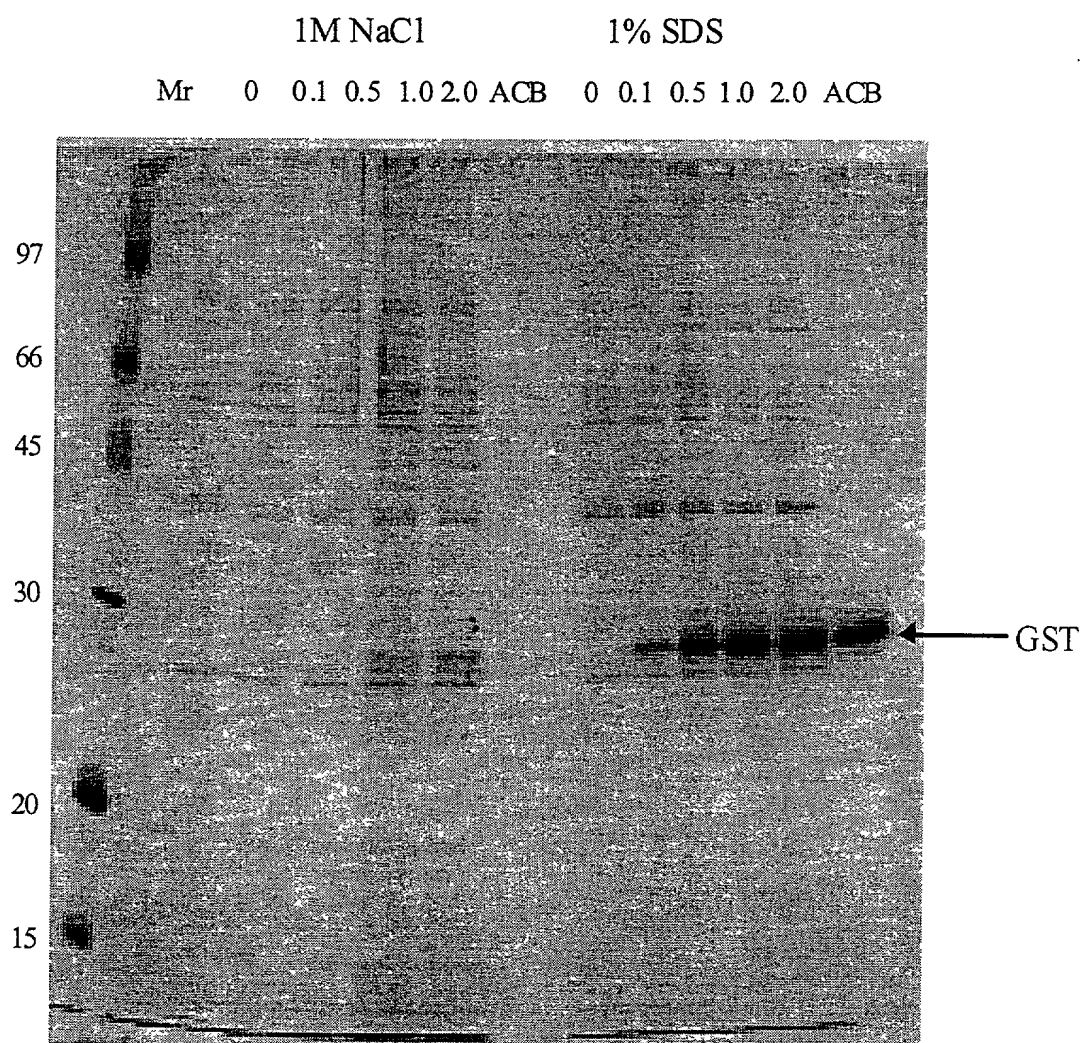


FIGURE 5 96ORF78 (GST removed)

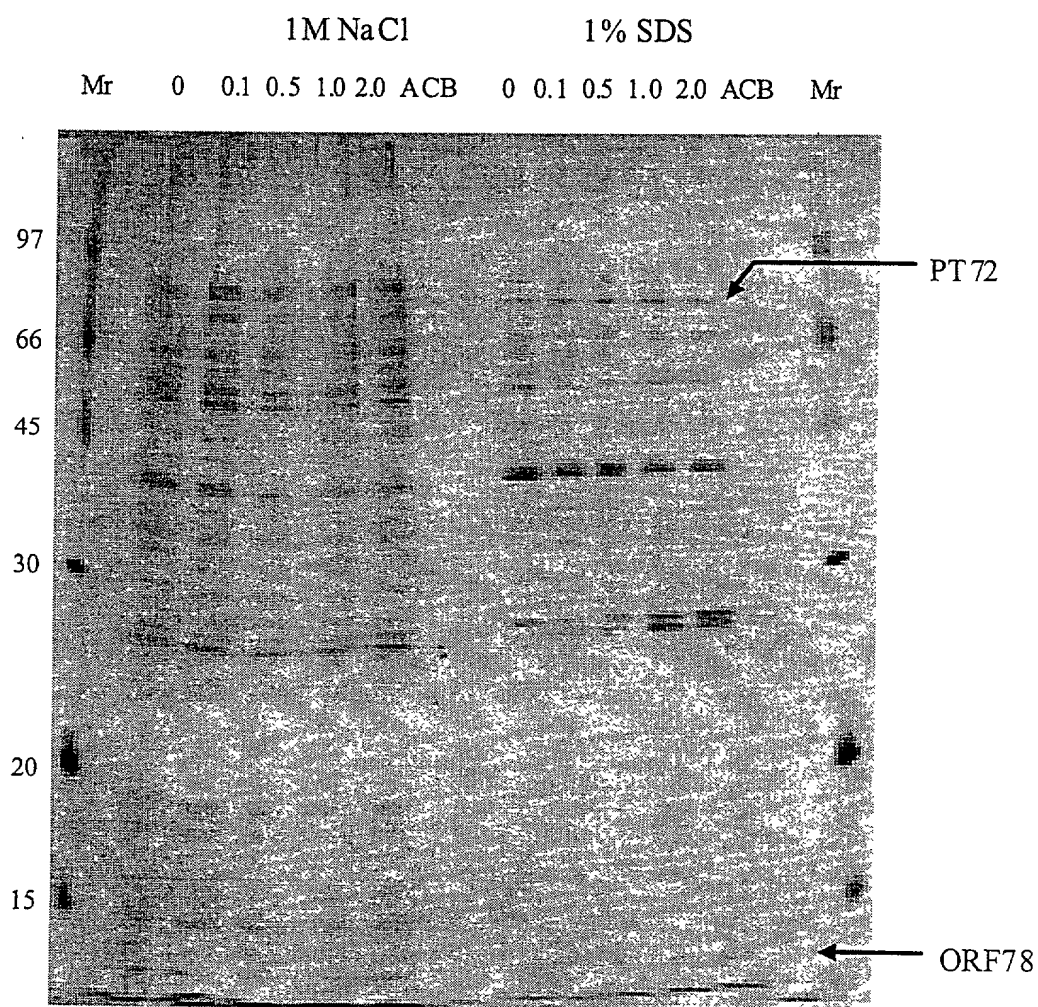
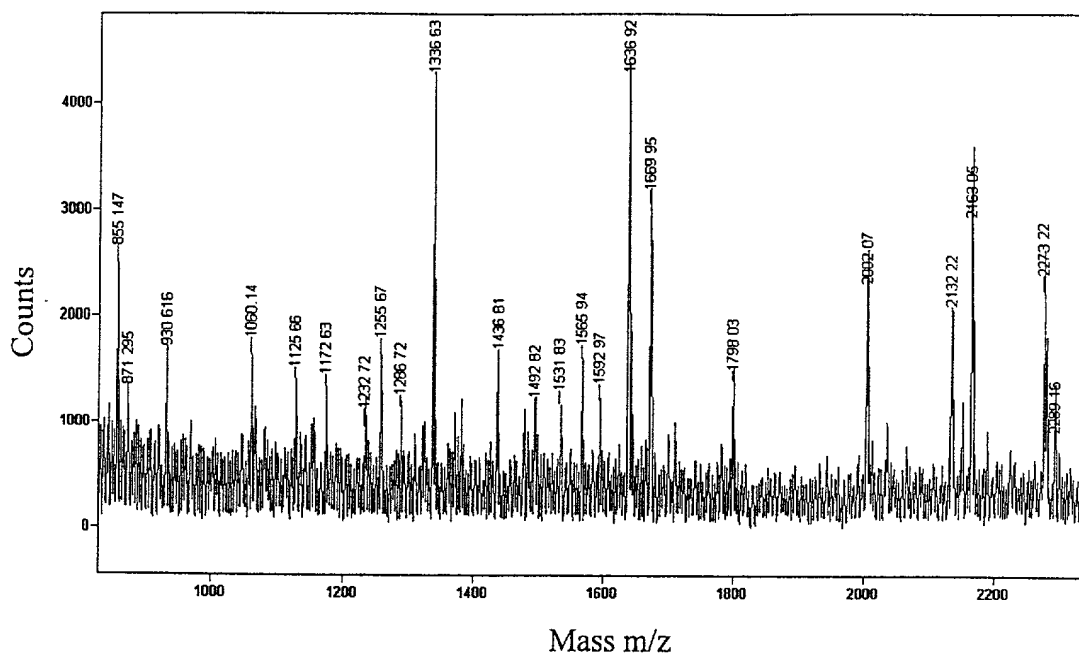


FIGURE 6



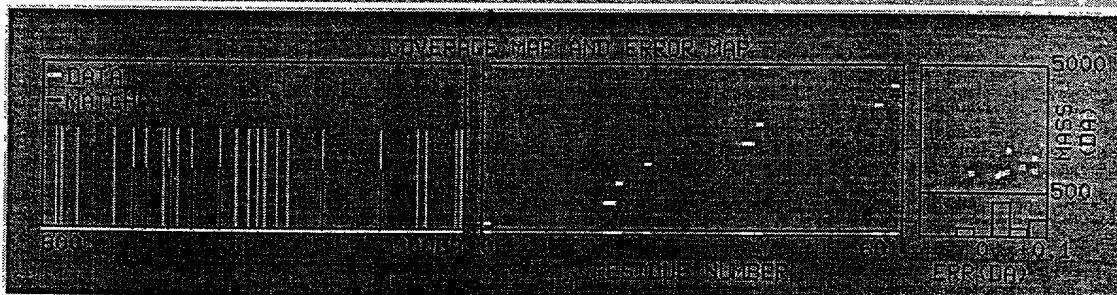
ouContig286: 82020 to 83822: Frame 3 601 aa

Sample ID : orf78 72 [Pass:0]

Measured peptides : 23

Matched peptides : 7

Min. sequence coverage: 14%



1124.649	M	1124.622	0.027	588	596	0	YYLQQIVAK
1171.623	M	1171.590	0.033	394	403	0	ELSHDISLMK
1171.623	M	1171.644	0.021	5	14	0	IDQSINEIK
1254.661	M	1254.620	0.041	563	573	0	GQETIESLNHK
1335.627	M	1335.536	0.091	193	202	0	NEENFSYYDR
1435.802	M	1435.734	0.068	233	244	0	YLNSPETPIFOK
1797.019	M	1796.930	0.089	177	192	1	KGYDIELAYEAGLLSR
2001.060	M	2001.016	0.044	374	390	1	VSILKDEIAHNDLSYER

855.147 871.295 930.616 1060.140 1232.717 1286.716 1492.822 1531.830 1565.943 1592.967
1636.921 1669.948 2132.217 2163.048 2273.222 2289.164

FIGURE 7A

A. Pfam HMM search results

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value
zf-CHC2	3	100	1	98	198.4	1.1e-55
Toprim	260	339	1	151	71.9	1.3e-17

Alignments of top-scoring domains:

zf-CHC2:
domain 1 of 1, from 3 to 100: score 198.4, E = 1.1e-55
*->ipeesIdelknriDIVdvisYVklkKkGrnYkgLCPFHdEKTSPFs
i++++I+e+k+++DI d++seYVkl+K+GrnY+gLCPFHdEKTSPF+
gi|133988 3 IDQSIINEIKDKTDILDVSEYVklEKRGRNYIGLCPFHdEKTSPFT 49

VspeKqfYhCFGCGagGdaIkFlmkyeklsFvEAvekLAdragidlpyek
Vs +Kq+ hCFGc++g+++ F ++++++sFvEA++L dr+++ +++e
gi|133988 50 VSEDKQICHCFGCKKGGNVFQFTQEIkdISFvEAveKELGDRVNVAVDIEA 99

g<-*
+
gi|133988 100 T 100

Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17

```

Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17
*->kvliiVEgpsdakalakalgpkskrkivyelpggkdgnavvaslGhlv
+++++ Eg++d+++ a+ +nvva++G+
gi|133988 260 DEIVLLEGFMDVIKSDTAGL-----KNVVATMGQTQ- 289

dLptpegyddkykwlwlpivdvkkgfepyqiefdqlckcskkidlkkeql
+++++
gi|133988 290 -----LSDEHI 295

kllkklakadevilatDpDreGeaiawkllellkpygpveleddkkvrr
++kl+++ + l++D+D +G ++++k + l+ +g +v++
gi|133988 296 TFIRKLTSN---ITLMFDGDFAGSEATLKTGQNLLQQGL-----NVFV 335

iflp<-*
i+lp
gi|133988 336 IQLP 339

```

FIGURE 7B

B. Optimal global alignment of amino acid sequences

Sequence 1 sp|O05338|PRIM_STAAU_DNA_PRIMASE (EC 2.7.7.-) - S. aureus. (572 letters)
Sequence 2 STAAU_R009 STAAU_R009 NT|1-1800| (599 letters)

Identical: 560/605 (92%), **Similar:** 564/605 (93%), **Gap:** 39/605 (6%)

seq1	1	M-----	-----IGLCPFHDEKTPSFTVSEDKQICHCF	27
seq2	1	LRIDQSIINEIKDKTDILDVSEYVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICHCF		60
seq1	28	GCKKGGNVFQFTQEI	KDISFVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQMIEMHE	87
seq2	61	GCKKGGNVFQFTQEI	KDISFVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQMIEMHE	120
seq1	88	LIQEFYYALT	KTVEGEQALTYLQERGETDALIKERGIGFAPDSSHFCHDFLQKKGYDIE	147
seq2	121	LIQEFYYALT	KTVEGEQALTYLQERGETDALIKERGIGFAPDSSHFCHDFLQKKGYDIE	180
seq1	148	LAYEAGLLSRNEENFSY	DRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIF	207
seq2	181	LAYEAGLLSRNEENFSY	DRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIF	240
seq1	208	QKRKLLYNLDKARKSIRKL	DEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEHITFIRK	267
seq2	241	QKRKLLYNLDKARKSIRKL	DEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEHITFIRK	300
seq1	268	LTSNITLMFDGDFAGSEAT	LKTGQHLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTTFV	327
seq2	301	LTSNITLMFDGDFAGSEAT	LKTGQNLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTAFV	360

Table 2

seq1	328	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKAINDVAPFFNVS	387
seq2	361	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVS	420
seq1	388	PEQLANEIQFNQAPANYYPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRREKAERAFLEKHL	447
seq2	421	PEQLANEIQFNQAPANYYPE-----DEYGGYIEPEPIGMAQFDNLSRQEKAEERAFLEKHL	474
seq1	448	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNI SDAVQYVNSNELRETLLI	507
seq2	475	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNI SDAVQYVNSNELRETLLI	534
seq1	508	SLEQYNLNGEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQQIVAK	567
seq2	535	SLEQYNLNDEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQQIVAK	594
seq1	568	NKERM	572
seq2	595	NKERM	599

[illegible]

Table 2. Sequence

seq1	414	APFFNVSPEQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAEAFCLKH	473
seq2	415	AEFSLSLSALHEQLSRQRERTKPREAPDGETARP----MLAKKLLPAFQNAERLLLAH	470
seq1	474	LMRDKDTFLNYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELRETL	533
seq2	471	MMRSRDVALVVQERIG-GRFNIEEHRALAAAYIYAFYEEGHEADPGALISRI-PGELQPLA	528
seq1	534	ISLEQYNLNDEPYENEIDDDYV-NVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIV	592
seq2	529	SDVSLLLIADDVSEQELEDYIRHVLNRPKWMLMKVKEQEKTEAERRKDFLTAARIAKEMI	588
seq1	593	AKNK--ERM	599
seq2	589	EMKKMLSSS	597

[illegible]

10

Sequence 1 STAAU_R009 (599 letters)
Sequence 2 gi|130908|sp|P02923|PRIM_ECOLI_DNA PRIMASE (581 letters)

Identical: 170/619 (27%), **Similar:** 294/619 (47%), **Gap:** 58/619 (9%)
seq1 1 L--RIDQSIINEIKDKTDILDVSEYVVKLEKGRGRNYIGLCPFHDEKTPSTTVSEDKOICH 58

58 60

118

119

178
175

235

234

295

294

352

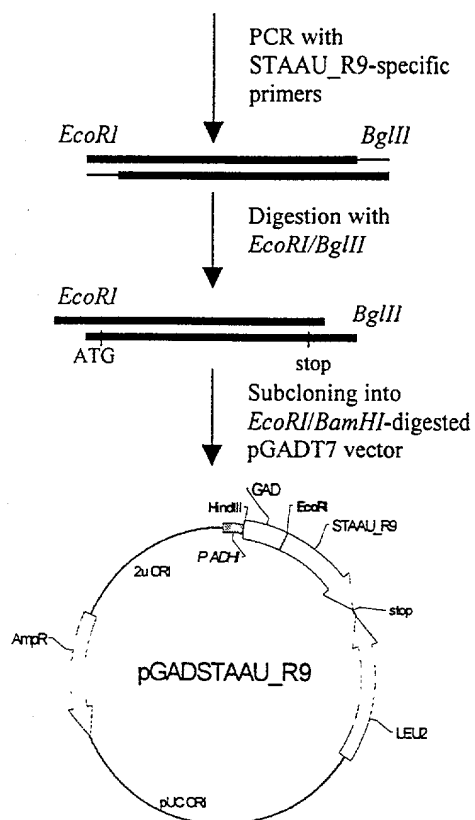
412 406

Table 2

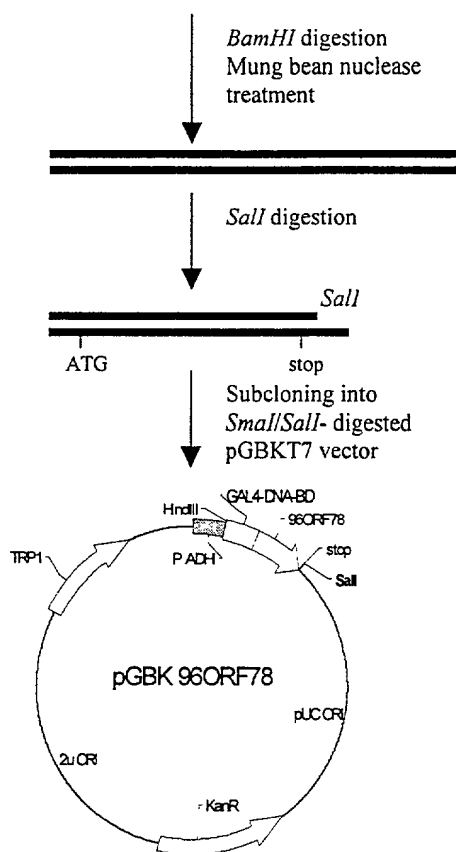
seq1	413	VAPFFNVSP	EQLANEIQF--NQAPANYYP	EDYGGYIEPEPIGMAQFDNLSRQEK	AERAF	470
seq2	407	LRIYLR---	QELGNKLGILDDSQ	LERLMPKAAESGVS	RPVP-----QLKR	454
seq1	471	LKHLMRDKD--	TFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNE			528
seq2	455	IGLLVQNPELATLVP	PLENLDENKLPGLG---LFREL	VNTCLS	QPGLTGQLLEHYRG	511
seq1	529	LRETLISLEQY-----	NLNDEPYENEIDDDYVNVINEKGQETIESLNHKL	REATR--IGD		580
seq2	512	NAATLEKLSMWDDIADKNIAEQ	FTDSLNMHMFDSLLELRQEELIA-----RERTHGLSNE			566
seq1	581	VELQYYYLQQI	VAKNKERM			599
seq2	567	ERLELWTLNQELAKK----				581

FIGURE 8

A- *Staphylococcus aureus* genomic DNA



B- 96pTMSMLacORF78



C-

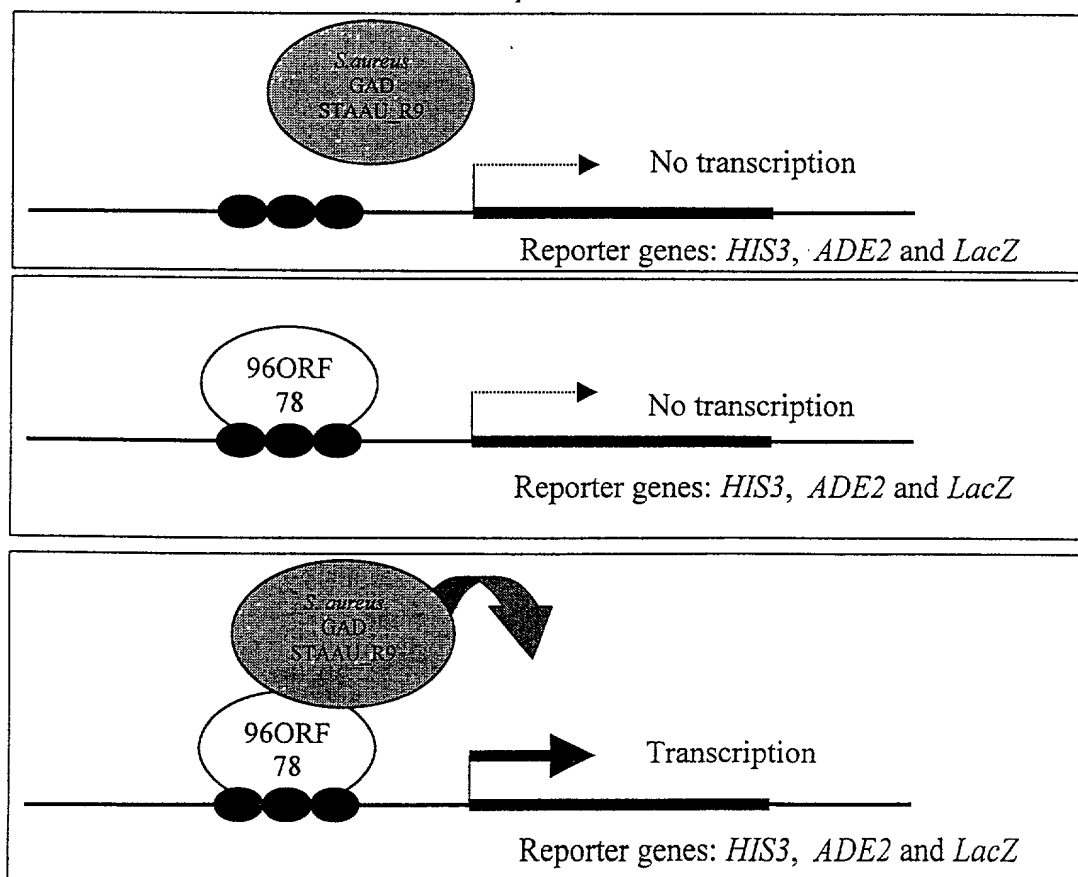
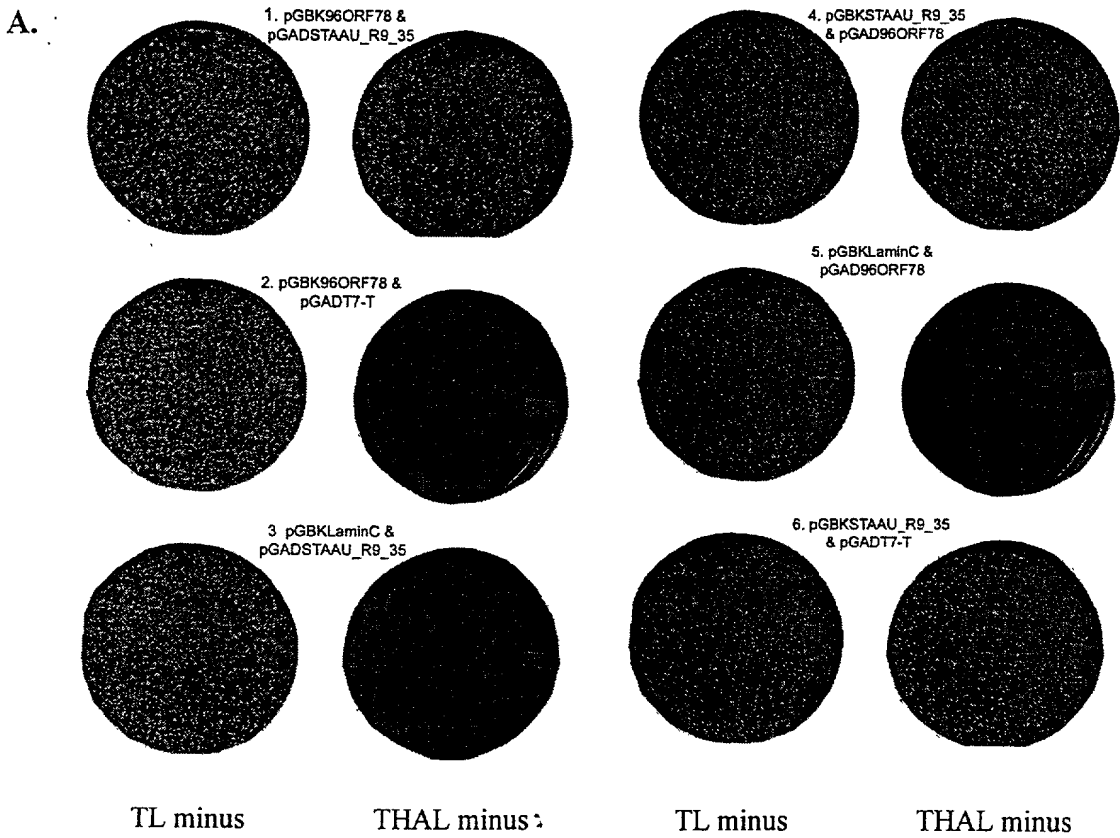
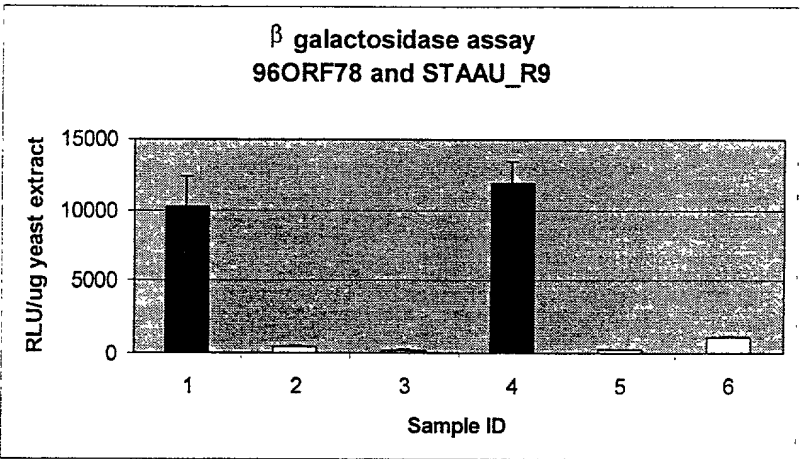


FIGURE 9



B.



Sample	Yeast co-transformants		RLU (avg)	SD
	Plasmid 1	Plasmid 2		
1	pGBK 96ORF78	pGADSTAAU_R9_35	10, 250	2, 080
2	pGBK 96ORF78	pGADT7-T	475	38
3	pGBK Lamin C	pGADSTAAU_R9_35	224	10
4	pGBKSTAAU_R9_35	pGAD 96ORF78	11, 935	1, 477
5	pGBK Lamin C	pGAD 96ORF78	243	12
6	pGBKSTAAU_R9_35	pGADT7-T	1, 121	37

FIGURE 10

A. Fragments of STAAU_R9

B.

Interaction with
96ORF78

1	599	Yes
35	599	Yes
35	342	No
229	402	No
229	599	Yes
380	599	Yes
380	449	No
380	490	No
380	530	No
380	561	No
449	599	Yes
490	599	Yes
530	599	Yes
561	599	Yes

SEQ ID NO: 6 STAAU_R9_561-599
AMINO ACID SEQUENCE

GQETIESLNHLKREATRIGDVELQKYLYLQQIVAKNKERM

SEQ ID NO: 5 STAAU_R9_1683-1800
NUCLEIC ACID SEQUENCE

GGACAAAGAAACAATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTA
GAATTACAAAATACTATTACAGCAAAATTGTTGCTAAGAATAAAGAACGCATGTAG

C.

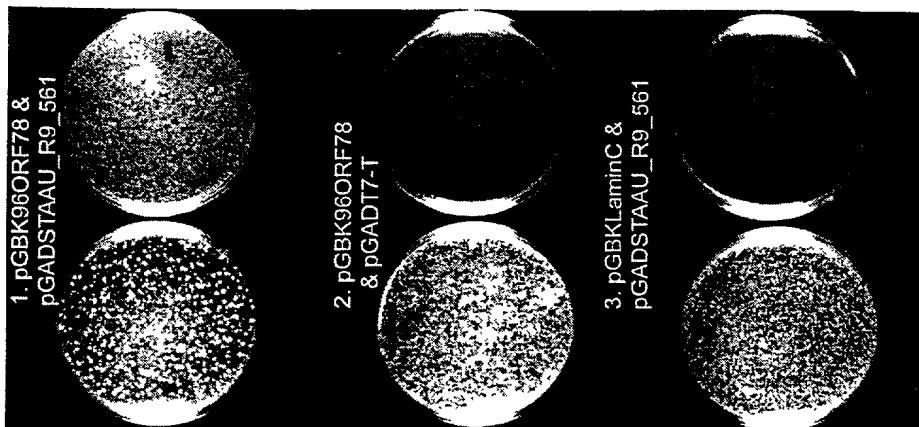


FIGURE 11

	Primer name	Primer sequence	Restriction site
SEQ ID NO: 8	R9_5E3	5'-ccggaattcTTGCGAATAGATCAATCG-3'	EcoRI
SEQ ID NO: 9	R9_3BG	5'-ggaagatcCTACATGCGTTCTTTATTC-3'	BglII
SEQ ID NO: 10	R9_5E	5'-ccggaattcATGATAGGTTTGTGTCCT-3'	EcoRI
SEQ ID NO: 11	R9_5E1	5'-ccggaattcCCAAAATACCTAAATAGTCC-3'	EcoRI
SEQ ID NO: 12	R9_5E2	5'-ccggaattcGCACATAATGACCTTTCA-3'	EcoRI
SEQ ID NO: 13	R9_342R	5'-cgcggatccATGCCTGATGGCAATTG-3'	BamHI
SEQ ID NO: 14	R9_402R	5'-ccatcgatGATTTTCATAAGCGAAATATC-3'	Clal
SEQ ID NO: 15	R9_449F	5'-ccggaattcCTGAGCCAATTGGTATGGC-3'	EcoRI
SEQ ID NO: 16	R9_449R	5'-cgcggatccctaAGGTTCAATGTAACCGCC-3'	BamHI
SEQ ID NO: 17	R9_490F	5'-ccggaattcAAGGATAACTTCACAAATCAG-3'	EcoRI
SEQ ID NO: 18	R9_490R	5'-cgcggatccctaCTTATCAACACTTTCATAATA-3'	BamHI
SEQ ID NO: 19	R9_530F	5'-ccggaattcAGAGAAACACTAATTAGCTTA-3'	EcoRI
SEQ ID NO: 20	R9_530R	5'-cgcggatccctaTCTCAACTCATTGTAATTAAAC-3'	BamHI
SEQ ID NO: 21	R9_561F	5'-ccggaattcGGACAAGAAACAATTGAGTC-3'	EcoRI
SEQ ID NO: 7	R9_561R	5'-cgcggatccctaTCCTTTTTCATTAAATAACATTG-3'	BamHI

A.

Cloning of SEQ ID NO: 2 amino acid fragments	Sense primer	Antisense primer
1-599	R9_5E3	R9_3BG
35-599	R9_5E	R9_3BG
35-342	R9_5E	R9_342R
229-402	R9_5E1	R9_402R
229-599	R9_5E1	R9_3BG
380-599	R9_5E2	R9_3BG
380-449	R9_5E2	R9_449R
380-490	R9_5E2	R9_490R
380-530	R9_5E2	R9_530R
380-561	R9_5E2	R9_561R
449-599	R9_449F	R9_3BG
490-599	R9_490F	R9_3BG
530-599	R9_530F	R9_3BG
561-599	R9_561F	R9_3BG

B.